

Serial Number: 09/720,096

☐ Changed a file from non-ASCII to ASCII

ENTERED

(PCT 09)

☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.☐ Edited a format error in the Current Application Data section, specifically:

Paper No. 10

DJS 3/19/02

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_☐ Added the mandatory heading and subheadings for "Current Application Data".☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_☐ Inserted mandatory headings, specifically: \_\_\_\_\_☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_☐ Edited identifiers where upper case is used but lower case is required, or vice versa.☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

PCT09

RAW SEQUENCE LISTING                      DATE: 03/06/2001  
PATENT APPLICATION: US/09/720,096              TIME: 13:30:07

Input Set : A:\Cpg.pto  
Output Set: N:\CRF3\03062001\I720096.raw

5 <110> APPLICANT: Dan Nilsson  
6     Thomas Janzen  
8 <120> TITLE OF INVENTION: Method of preventing bacteriophage  
9     infection of bacterial cultures  
12 <130> FILE REFERENCE: 21134 PC 1  
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/720,096  
C--> 14 <141> CURRENT FILING DATE: 2000-12-21  
14 <150> PRIOR APPLICATION NUMBER: PA 1998 00878  
15 <151> PRIOR FILING DATE: 1998-07-03  
17 <150> PRIOR APPLICATION NUMBER: US 60/091,735  
18 <151> PRIOR FILING DATE: 1998-07-06  
20 <160> NUMBER OF SEQ ID NOS: 6  
22 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 32  
26 <212> TYPE: DNA  
27 <213> ORGANISM: Artificial Sequence  
29 <220> FEATURE:  
30 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with  
31     deletion in thyA from strain CHCC373  
33 <400> SEQUENCE: 1  
34     tataatctgc agggtcacac tatcagtaat tg 32  
36 <210> SEQ ID NO: 2  
37 <211> LENGTH: 33  
38 <212> TYPE: DNA  
39 <213> ORGANISM: Artificial Sequence  
41 <220> FEATURE:  
42 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with  
43     deletion in thyA from strain CHCC373  
45 <400> SEQUENCE: 2  
46     tattttaagc ttcacagtct gctattttga ttc 33  
48 <210> SEQ ID NO: 3  
49 <211> LENGTH: 32  
50 <212> TYPE: DNA  
51 <213> ORGANISM: Artificial Sequence  
53 <220> FEATURE:  
54 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with  
55     deletion in thyA from strain CHCC373  
57 <400> SEQUENCE: 3  
58     taaattaagc ttcgcagaca agatttttaa ac 32  
61 <210> SEQ ID NO: 4  
62 <211> LENGTH: 32  
63 <212> TYPE: DNA  
64 <213> ORGANISM: Artificial Sequence  
66 <220> FEATURE:  
67 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with  
68     deletion in thyA from strain CHCC373

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/720,096

DATE: 03/06/2001  
TIME: 13:30:07

Input Set : A:\Cpg.pto  
Output Set: N:\CRF3\03062001\I720096.raw

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70 <400> SEQUENCE: 4
71      atttaagtcg acgggtcata gtccacaagt tc 32
73 <210> SEQ ID NO: 5
74 <211> LENGTH: 18
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: Sequencing primer used for the verification of the
80      construction of plasmid with deletion in thyA from
81      strain CHCC373.
83 <400> SEQUENCE: 5
84      gactgttgcc ccatagcg 18
86 <210> SEQ ID NO: 6
87 <211> LENGTH: 20
88 <212> TYPE: DNA
89 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
92 <223> OTHER INFORMATION: Sequencing primer used for the verification of the
93      construction of plasmid with deletion in thyA from
94      strain CHCC373.
96 <400> SEQUENCE: 6
97      gcttcgattt tagtatatgg 20
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/720,096

DATE: 03/06/2001

TIME: 13:30:08

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\03062001\I720096.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

PCT 09

RAW SEQUENCE LISTING                      DATE: 02/22/2001  
 PATENT APPLICATION: US/09/720,096        TIME: 09:42:35

Input Set : A:\Sequence List.asc  
 Output Set: N:\CRF3\02222001\I720096.raw

6 <110> APPLICANT: Dan Nilsson  
 7        Thomas Janzen  
 9 <120> TITLE OF INVENTION: Method of preventing bacteriophage  
 10       infection of bacterial cultures  
 13 <130> FILE REFERENCE: 21134 PC 1  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/720,096  
 C--> 15 <141> CURRENT FILING DATE: 2000-12-21  
 15 <150> PRIOR APPLICATION NUMBER: PA 1998 00878  
 16 <151> PRIOR FILING DATE: 1998-07-03  
 18 <150> PRIOR APPLICATION NUMBER: US 60/091,735  
 19 <151> PRIOR FILING DATE: 1998-07-06  
 21 <160> NUMBER OF SEQ ID NOS: 6  
 23 <170> SOFTWARE: FastSEQ for Windows Version 3.0

# ERRORED SEQUENCES

25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 32  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Artificial Sequence  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with  
 32       deletion in thyA from strain CHCC373  
 34 <400> SEQUENCE: 1  
 W--> 35        tataatctgc agggtcacac tatcagtaat tg  
 E--> 36 32  
 38 <210> SEQ ID NO: 2  
 39 <211> LENGTH: 33  
 40 <212> TYPE: DNA  
 41 <213> ORGANISM: Artificial Sequence  
 43 <220> FEATURE:  
 44 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with  
 45       deletion in thyA from strain CHCC373  
 47 <400> SEQUENCE: 2  
 W--> 48        tattttaagc ttcacagtct gctattttga ttc  
 E--> 49 33  
 51 <210> SEQ ID NO: 3  
 52 <211> LENGTH: 32  
 53 <212> TYPE: DNA  
 54 <213> ORGANISM: Artificial Sequence  
 56 <220> FEATURE:  
 57 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with  
 58       deletion in thyA from strain CHCC373  
 60 <400> SEQUENCE: 3  
 W--> 61        taaattaagc ttgcagaca agatttttaa ac  
 E--> 62 32

Does Not Comply  
 Corrected Diskette Needed

"Wrapped" Nucleics  
 End of line nucleic  
 numbers "wrapped"  
 down to next line.

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/720,096  
 DATE: 02/22/2001  
 TIME: 09:42:35

Input Set : A:\Sequence List.asc  
 Output Set: N:\CRF3\02222001\I720096.raw

```

65 <210> SEQ ID NO: 4
66 <211> LENGTH: 32
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
71 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with
72   deletion in thyA from strain CHCC373
74 <400> SEQUENCE: 4
W--> 75      atttaagtgc acggtccata gtccacaagt tc
E--> 76 32 -----
78 <210> SEQ ID NO: 5
79 <211> LENGTH: 18
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial Sequence
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Sequencing primer used for the verification of
85   the
86   construction of plasmid with deletion in thyA
87   from
W--> 88   strain CHCC373.
90 <400> SEQUENCE: 5
W--> 91      gactgttgcc ccatagcg
E--> 92 18 -----
94 <210> SEQ ID NO: 6
95 <211> LENGTH: 20
96 <212> TYPE: DNA
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Sequencing primer used for the verification of
101   the
102   construction of plasmid with deletion in thyA
103   from
W--> 104   strain CHCC373.
106 <400> SEQUENCE: 6
W--> 107      gcttcgattt tagtatatgg
W--> 108 20 -----
W--> 110 Path: DOCSOPEN\WASHINGT\08360\54337\000009\42Y001!.DOC
E--> 111 doc #: 190440; v. 1
E--> 112 doc name: sequence List (54337.9)

```

*wrapped nucleic number refer to p1*

*Text is "wrapped" down, over the limit of 4 lines for <223>*

*wrapped nucleic number*

*Text is "wrapped" down, over limit of 4 lines. for <223>*

*wrapped nucleic number*

↘ Delete extraneous material from the end of the file.

## VERIFICATION SUMMARY

DATE: 02/22/2001

PATENT APPLICATION: US/09/720,096

TIME: 09:42:36

Input Set : A:\Sequence List.asc

Output Set: N:\CRF3\02222001\I720096.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No  
 L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:35 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4  
 L:36 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:36 M:252 E: No. of Seq. differs, <211>LENGTH:Input:32 Found:0 SEQ:1  
 L:48 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4  
 L:49 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
 L:49 M:252 E: No. of Seq. differs, <211>LENGTH:Input:33 Found:0 SEQ:2  
 L:61 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4  
 L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:62 M:252 E: No. of Seq. differs, <211>LENGTH:Input:32 Found:0 SEQ:3  
 L:75 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4  
 L:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
 L:76 M:252 E: No. of Seq. differs, <211>LENGTH:Input:32 Found:0 SEQ:4  
 L:88 M:259 W: Field exceeds allowed number of lines, <223> Other Information:  
 L:91 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2  
 L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:92 M:252 E: No. of Seq. differs, <211>LENGTH:Input:18 Found:0 SEQ:5  
 L:104 M:259 W: Field exceeds allowed number of lines, <223> Other Information:  
 L:107 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2  
 L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6  
 L:110 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2  
 L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6  
 L:111 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:8 SEQ:6  
 L:111 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
 L:111 M:112 C: (48) String data converted to lower case,  
 L:112 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6  
 L:112 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
 L:112 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6  
 M:254 Repeated in SeqNo=6  
 L:112 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:18  
 M:112 Repeated in SeqNo=6  
 L:112 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:31 SEQ:6